

Localisation of exonic SNPs on one of the three alternative forms:

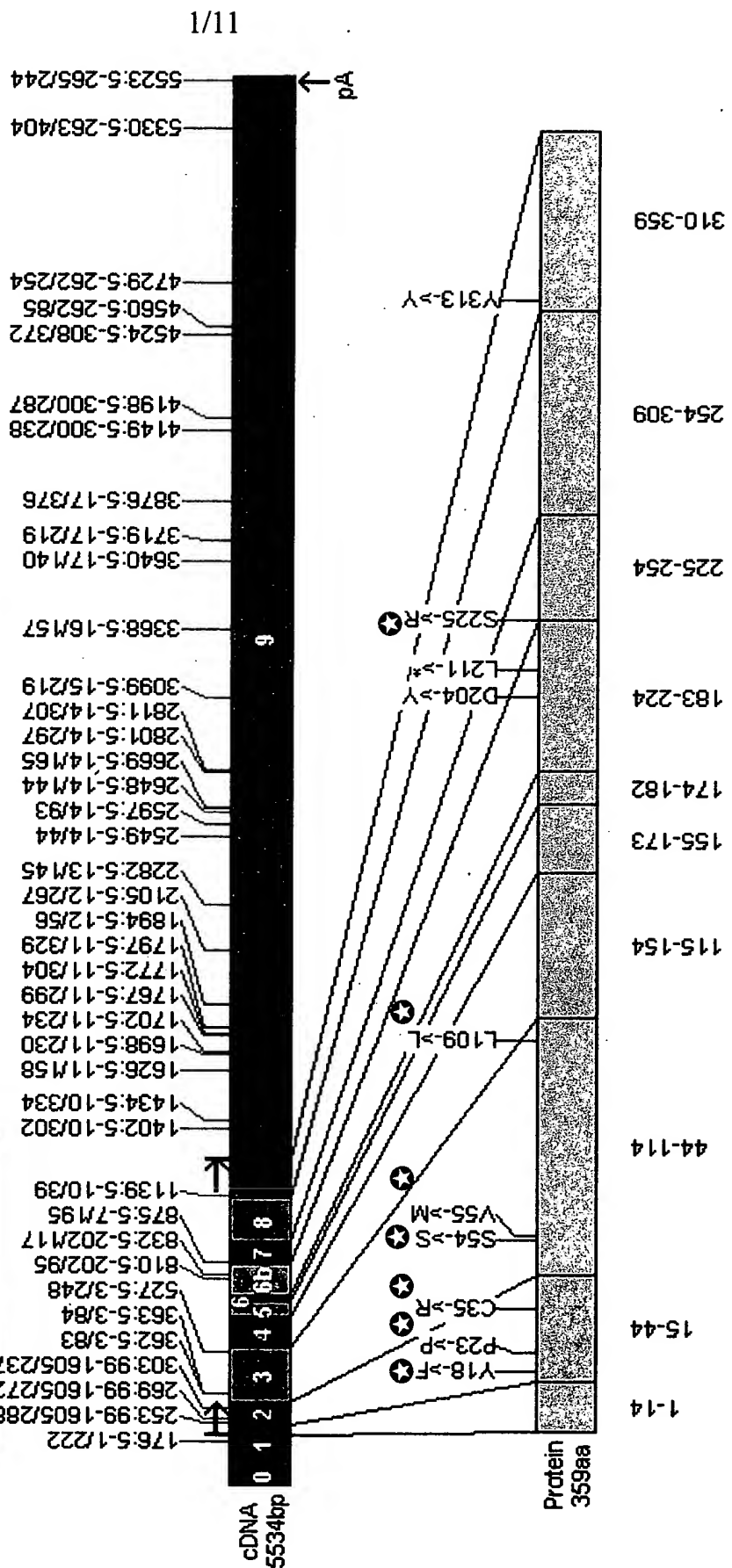


Figure 1A

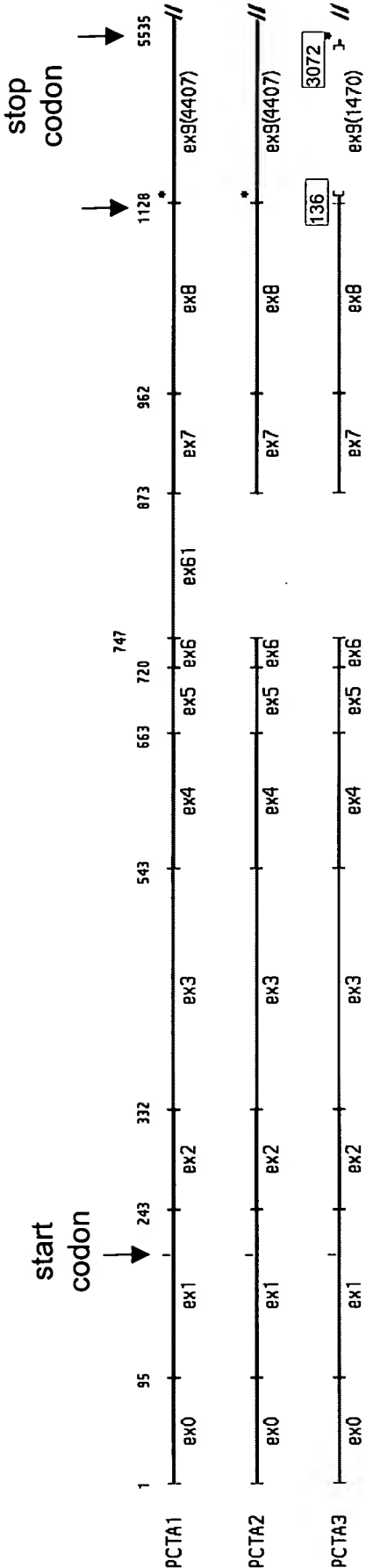


FIG. 1B



3/11

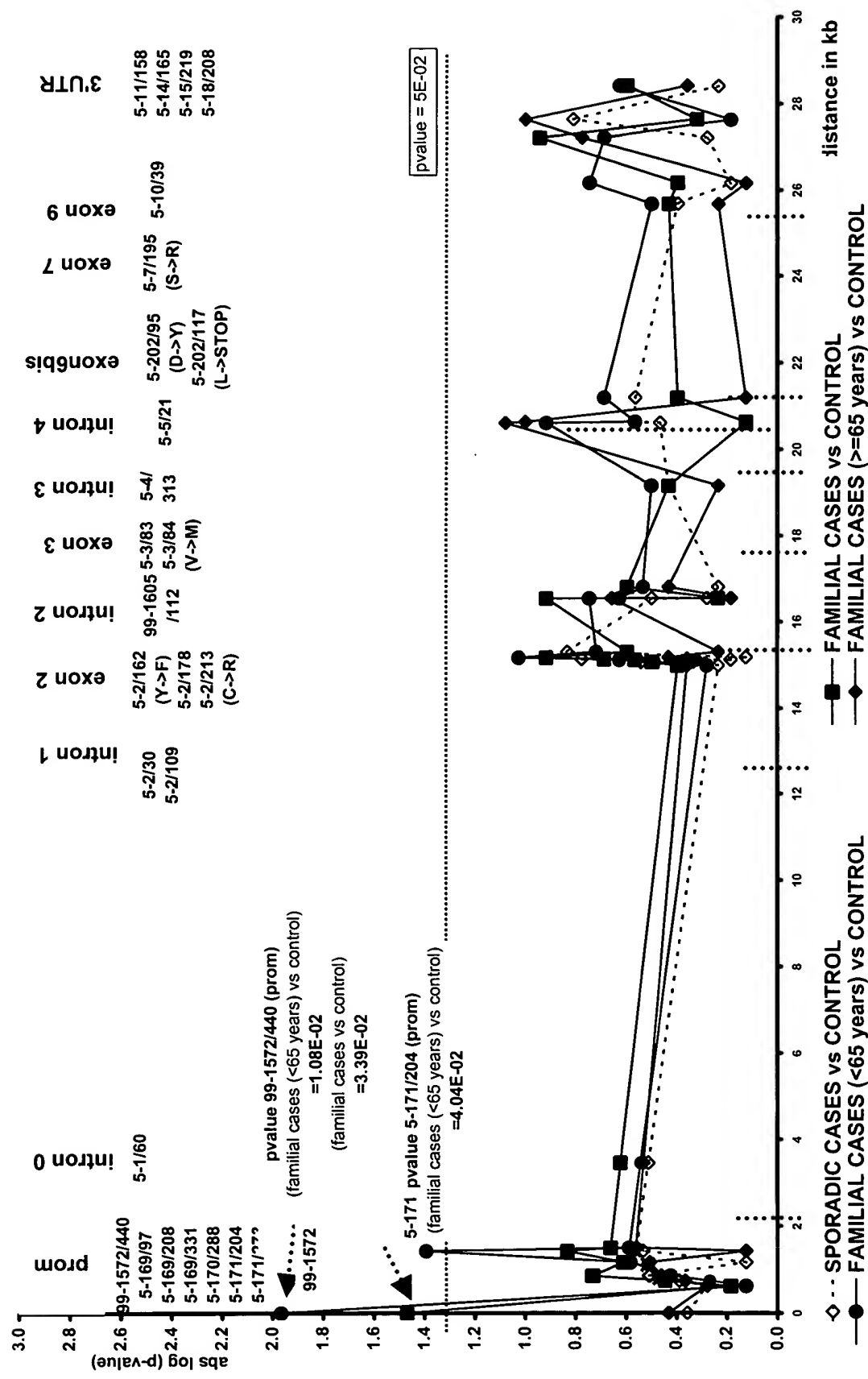


FIG. 2



4/11

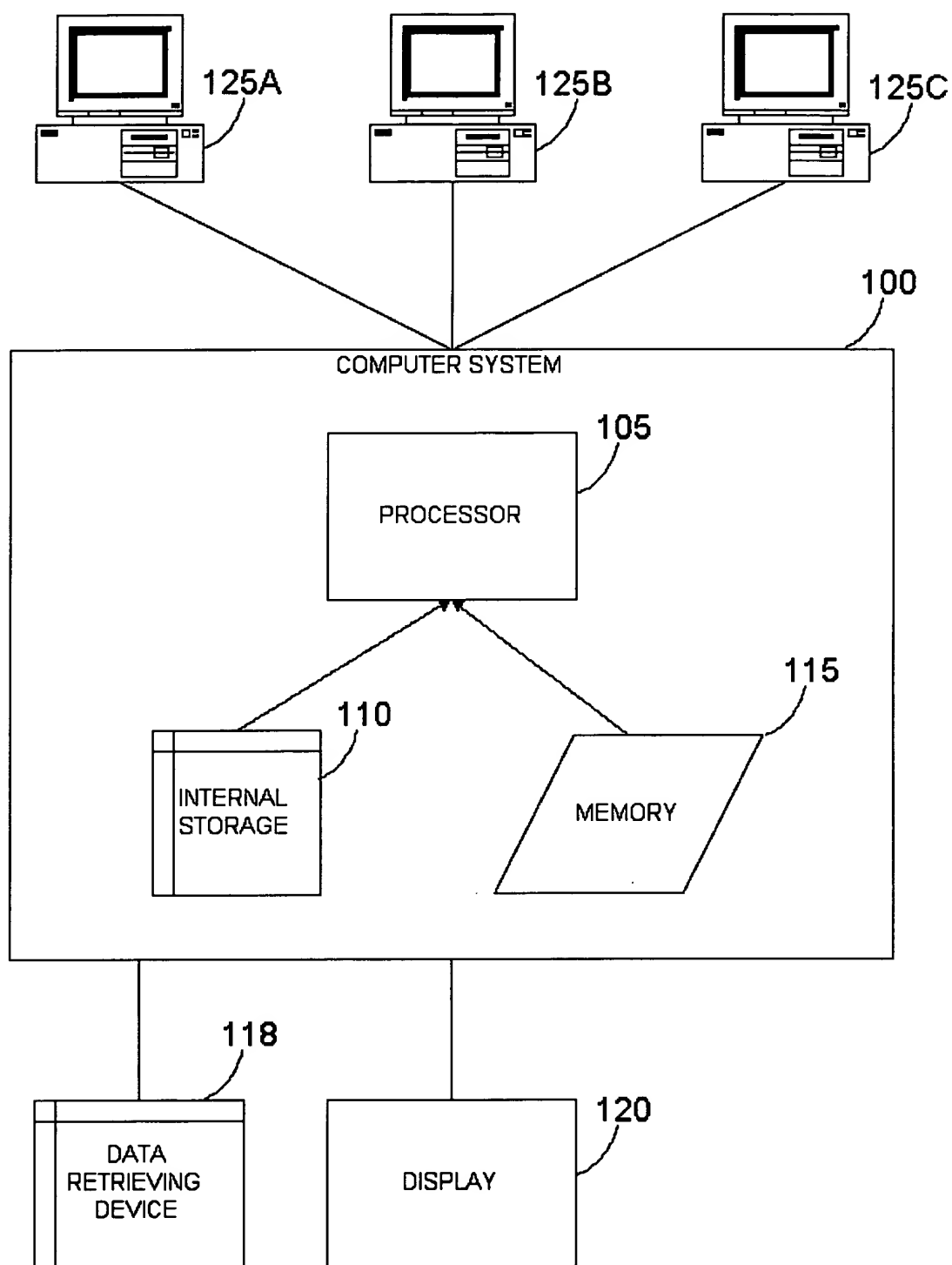


FIG. 3

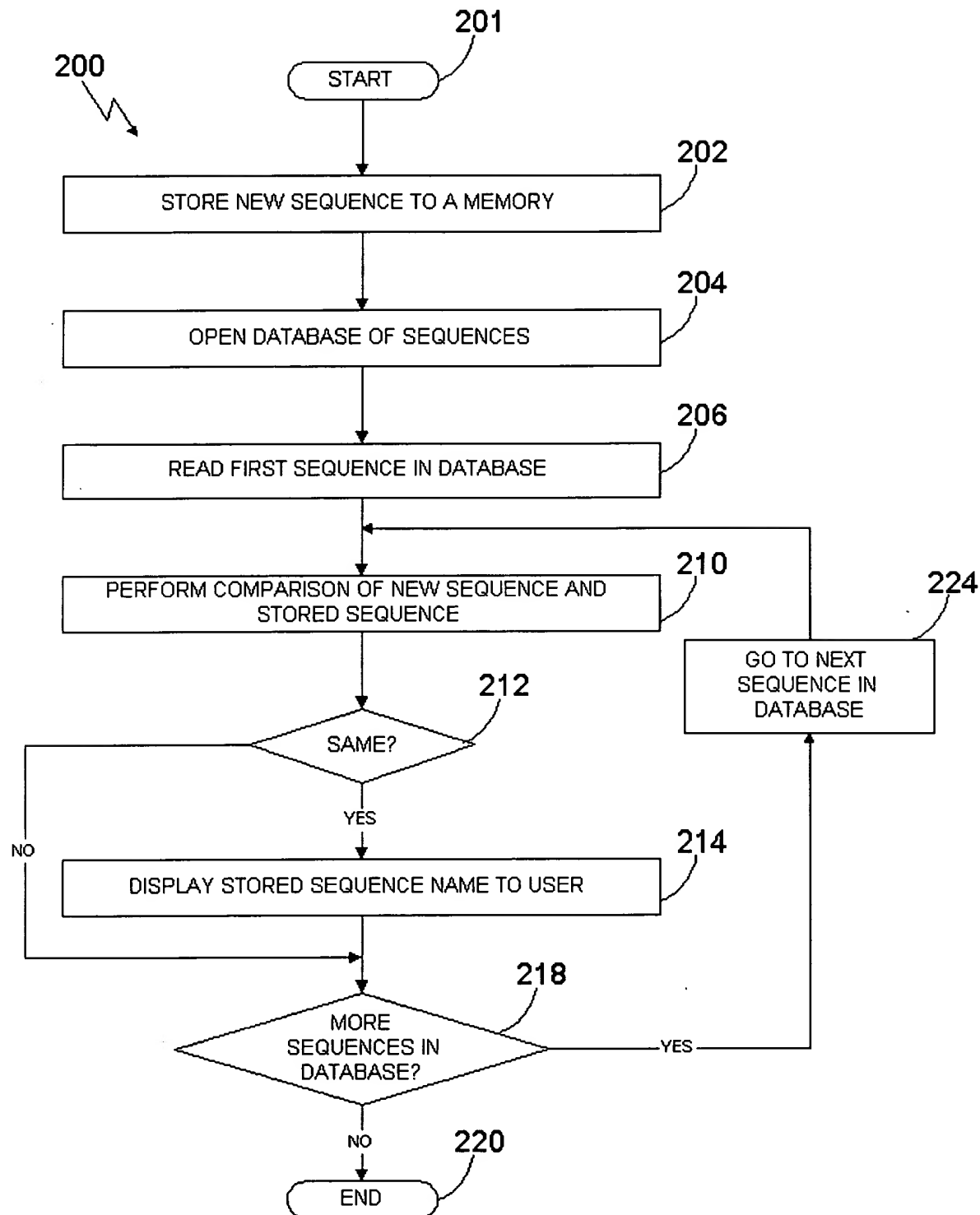


FIG. 4



6/11

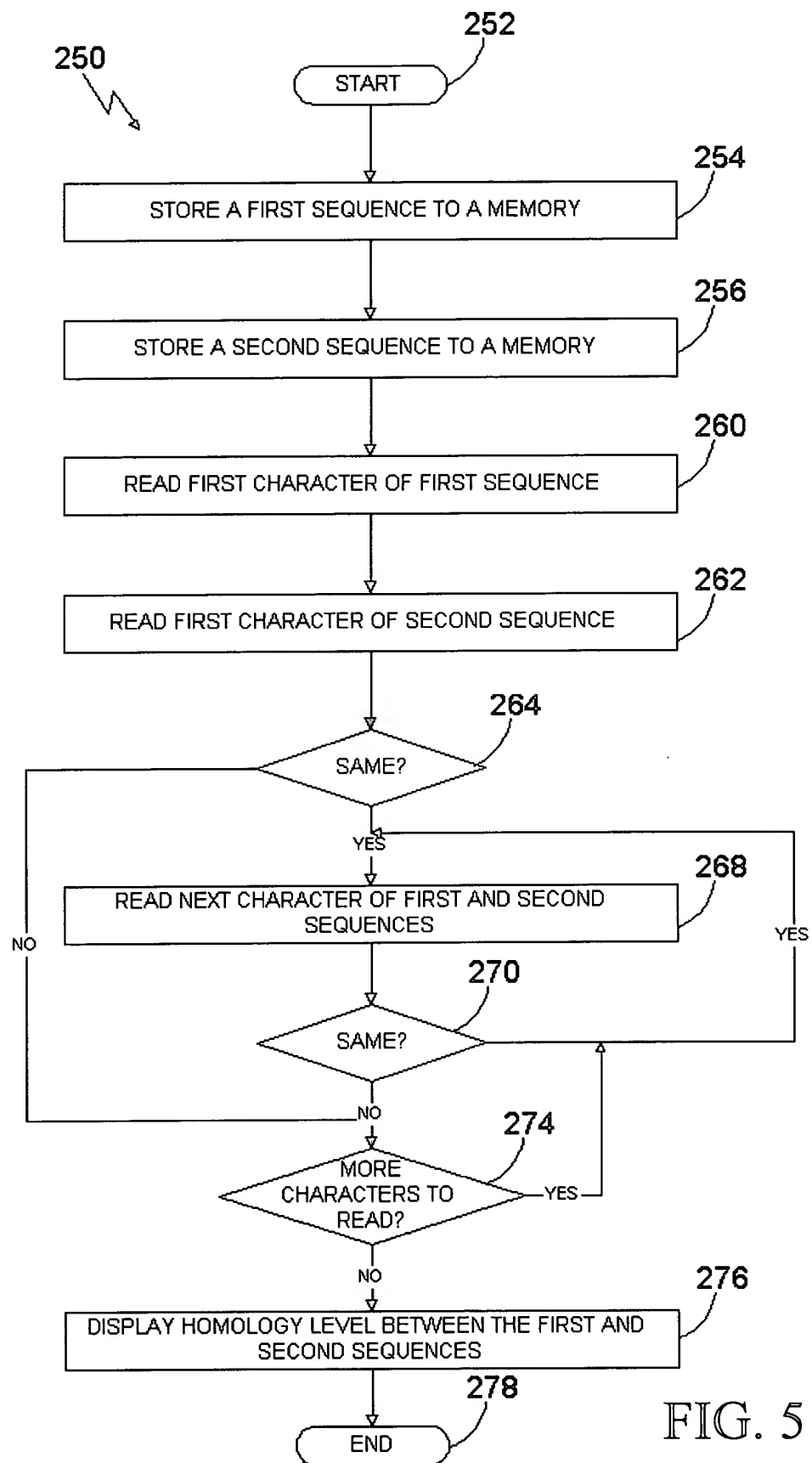


FIG. 5

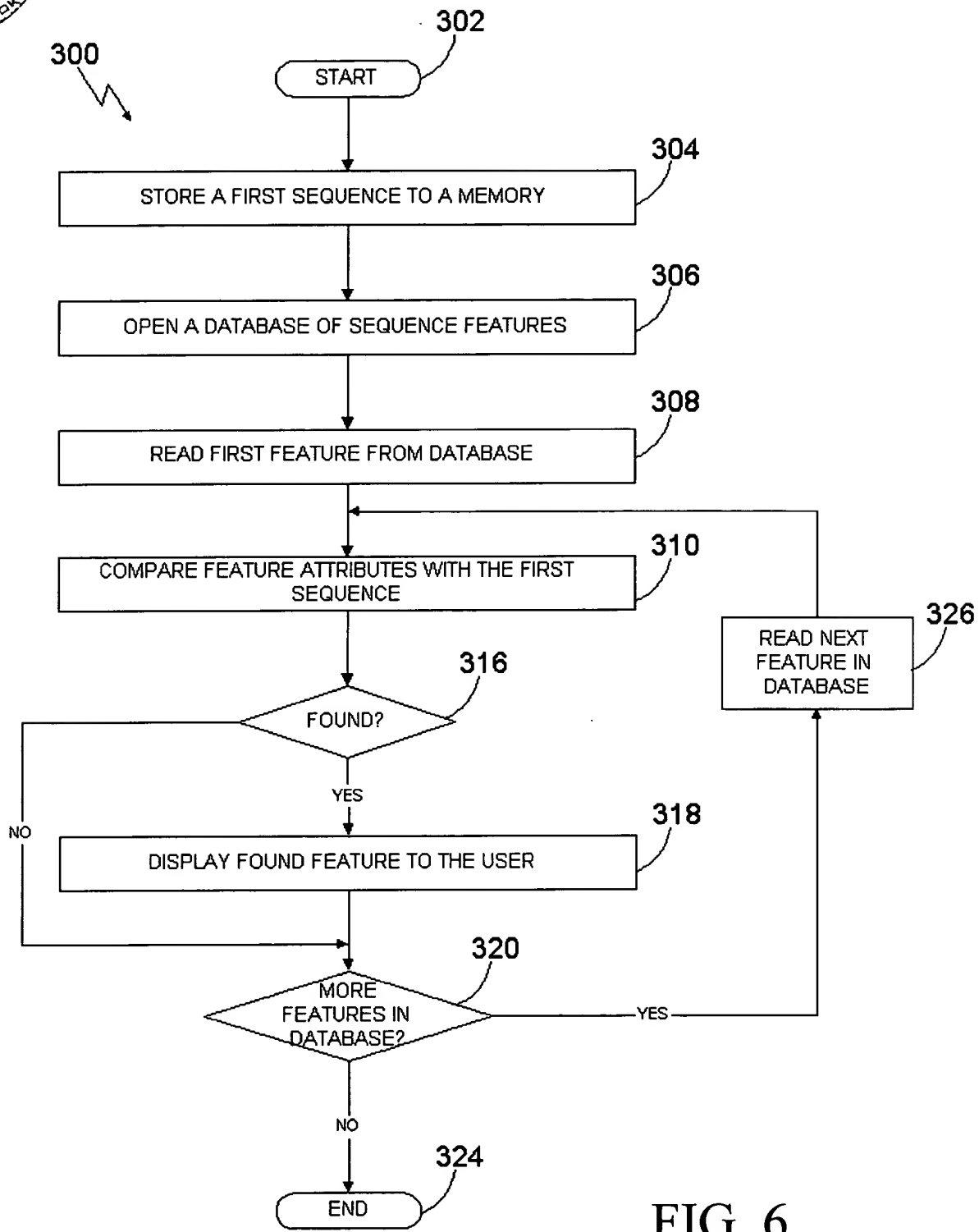


FIG. 6

8/11

	1					50
leg2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
leg1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA.var	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA.mus	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal9-1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
leg7	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal4	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Consensus	-----	-----	-----	-----	-----	-----
	51					100
leg2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
leg1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA.var	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA.mus	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal9-1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
leg7	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal4	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~M
Consensus	-----	-----	-----	-----	-----	-----
	101					150
leg2	~~~~~	~~~~~MTGELE	VKNMDMKPGS	TLKITGSIAD	.GTDGFVINL	
leg1	~~~~~	~~~~~ACGLV	ASNLNLPKGE	CLRVGEVAP	.DAKSFVLNL	
PCTA	MLSLNNLQNI	IYNPVIPIYVG	TIPDQLDPGT	LIVICGHV.P	SDADRFQVDL	
PCTA.var	MLSLNNLQNI	IYNPVIPIYVG	TIPDQLDPGT	LIVICGHV.P	SDADRFQVDL	
PCTA.mus	MLSLNNLQNI	IYNPIPIYVG	TITEQLKPGS	LIVIRGHV.P	KDSERFQVDF	
gal9-1	~MAFSGSQAP	YLSPAVPFSG	TIQGGQLDGL	QITVNGTVLS	SSGTRFAVNF	
gal	~MAFSGSQAP	YLSPAVPFSG	TIQGGQLDGL	QITVNGTVLS	SSGTRFAVNF	
leg7	~~~~~	~~~~~SNVPHKS	SLPEGIRPGT	VLRIRG.LVP	PNASRFHVNL	
gal4	AYVPAPGYQP	TYNPTLPYYQ	PIPGGLNVGM	SVYIQG.VAS	EHMKRFFVNF	
Consensus	-----	---P--P---	-IP-GL-PG-	---I-G-V-P	--A-RF-VNL	

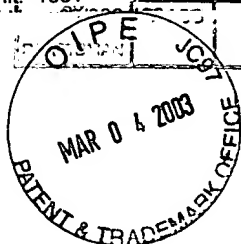
FIG. 7A



9/11

	151	200
leg2	GQGTD..... KLNLFHFNPRF	S....ESTIV CNSLDGSMWG QEQRDHLCPF
leg1	GKDSN..... NLCLHFHFNPRF	NAHGDANTIV CNSKDGGAWG TEQREAVFPF
PCTA	QNGSSVKPRA DVAFHFNPRF	K.RAGC. IV CNTLINEKWG REEITYDTPF
PCTA.var	QNGSSVKPRA DVAFHFNPRF	K.RAGC. IV CNTLINEKWG REEITYDTPF
PCTA.mus	QLGNSLKPRA DVAFHFNPRF	K.RSSC. IV CNTLTQEKWG WEEITYDMPF
gal9-1	QTGFS...GN DIAFHFNPRF	E.DGGY. VV CNTRQNGSWG PEERKTHMPF
gal	QTGFS...GN DIAFHFNPRF	E.DGGY. VV CNTRQNGSWG PEERRTHMPF
leg7	LCGEE..QGS DAALHFHFNPRF	D..TSE. VV FNSKEQGSWG REERGPVVPF
gal4	VVGQD..PGS DVAFHFNPRF	D.GWDK..VV FNTLQGGKWG SEERKRSMFP
Consensus	--G-----G- D-AFHFNPRF	-----VV CNT---G-WG -EER----PF
	201	250
leg2	SPGSEVKFTV TFESDKFKVK	LPDGHELTFP NRLG.HSHLS YLSVRGGFNM
leg1	QPGSVAEVC I TFDQANLTVK	LPDGYEFKFP NRLN.LEAIN YMAADGDFKI
PCTA	KREKSFEIVI MVLKDKFQVA	VNGKHTLLYG HRI.GPEKID TLGIYGVNI
PCTA.var	KREKSFEIVI MVLKDKFQVA	VNGKHTLLYG HRI.GPEKID TLGIYGVNI
PCTA.mus	RREKSFEIVF MVLKDKFQVA	VNGRHVLLYA HRI.SPEQID TVGIYGVNI
gal9-1	QKGMFPDLCF LVQSSDFKVM	VNGILFVQYF HRV.PFHRVD TISVNGSVQL
gal	QKGMFPDLCF LVQSSDFKVM	VNGILFVQYF HRV.PFHRVD TIFVNGSVQL
leg7	QRGQPFEVLI IASDDGFKAV	VGDAQYHHFR HRL.PLARVR LVEVGGDVQL
gal4	KKGAAFELVF IVLAEHYKVV	VNGNPFYEYG HRL.PLQMVT HLQVDGDLQL
Consensus	--G--FE--- -V--D-FKV-	VNG-----Y- HRL-PL--V- ---V-GDVQL
	251	300
leg2	SSFKLKE----	-----
leg1	KCVAFD-----	-----
PCTA	HSIGFSFSSD LQSTQASSLE	LTEISRENV KSGTPQL...
PCTA.var	HSIGFSFSSD LQSTQASSLE	LTEISRENV KSGTPQLPSN RGGDISKIAP
PCTA.mus	HSIGFRFSSD LQSMETSALG	LTQINRENIQ KPGKLQL...
gal9-1	SYISFQNPRT VPVQPAFSTV	PFSQPVCPPP RPRGRRQKPP GVWPANPAPI
gal	SYISFQ....PP GVWPANPAPI
leg7	DSVRIF-----	-----
gal4	QSINFI....GGQP .LRPQGPPMM
Consensus	-SI-F-----	-----

FIG. 7B



10/11

	301				350
leg2	-----	-----	-----	-----	-----
leg1	-----	-----	-----	-----	-----
PCTAS	..LPFAARLN	TPMGPGRTVV
PCTA.var	RTVYTKSKDS	TVNHTLTCTK	IPPMNYVSKS	..LPFAARLN	TPMGPGRTVV
PCTA.musS	..LPFEARLN	ASMGPGRTVV
gal9-1	TQTVIHTVQS	APGQMFSTPA	IPPMYHPHA	YPMPFITTIL	GGLYPSKSIL
gal	TQTVIHTVQS	APGQMFSTPA	IPPMYHPHA	YPMPFITTIL	GGLYPSKSIL
leg7	-----	-----	-----	-----	-----
gal4	PPYPGPGHCH	QQLNSLPTME	GPPTFNP...	.PVPYFGRLQ	GGLTARRTII
Consensus	-----	-----	-----	---P-----	-----
	351				400
leg2	-----	-----	-----	-----	-----
leg1	-----	-----	-----	-----	-----
PCTA	VKGEVNANAK	SFNVDLLAGK	SKDIALHLNP	RLNIKAFVRN	SFLQESWGEE
PCTA.var	VKGEVNANAK	SFNVDLLAGK	SKDIALHLNP	RLNIKAFVRN	SFLQESWGEE
PCTA.mus	IKGEVNTNAR	SFNVDLVAGK	TRDIALHLNP	RLNVKAFVRN	SFLQDAWGEE
gal9-1	LSGTVLPSAQ	RFHIN..LCS	GNHIAFHLNP	RFDENAVVRN	TQIDNSWGSE
gal	LSGTVLPSAQ	RFHIN..LCS	GNHIAFHLNL	RFDENAVVRN	TQIDNSWGSE
leg7	-----	-----	-----	-----	-----
gal4	IKGYVPPTGK	SFAINFKVGS	SGDIALHINP	RMGNGTVVRN	SLLNWSWGSE
Consensus	--G-V-----	-F-----	---IA-H-N-	R-----VRN	-----WG-E
	401				450
leg2	-----	-----	-----	-----	-----
leg1	-----	-----	-----	-----	-----
PCTA	ERNIT.SFPF	SPGMYFEMII	YCDVREFKVA	VNGVHSLEYK	HRFKELSSID
PCTA.var	ERNIT.SFPF	SPGMYFEMII	YCDVREFKVA	VNGVHSLEYK	HRFKELSSID
PCTA.mus	ERNIT.CFPF	SSGMYFEMII	YCDVREFKVA	INGVHSLEYK	HRFKDLSSID
gal9-1	ERSLPRKMPF	VRGQSFSVWI	LCEAHCLKVA	VDGQHLFEYY	HRLRNLPTIN
gal	ERSLPRKMPF	VRGQSFSVWI	LCGAHCLKVA	VDGQHLFEYY	HRLRNLPTIN
leg7	-----	-----	-----	-----	-----
gal4	EKKITHN..PF	GPGQFFDL SI	RCGLDRFKVY	ANGQHLFDFA	HRLSAFORVD
Consensus	E-----PF	--G--F---I	-C-----KV-	--G-H-----	HR-----

FIG. 7C



	451	466
leg2	~~~~~	~~~~~
leg1	~~~~~	~~~~~
PCTA	TLEINGDIHL	LEVRSW
PCTA.var	TLEINGDIHL	LEVRSW
PCTA.mus	TLSDVGDIRL	LDVRSW
gal9-1	RLEVGGDIQL	THVQT~
gal	RLEVGGDIQL	THVQT~
leg7	~~~~~	~~~~~
gal4	TLEIQGDVTL	SYVQI~
Consensus	-L---GD--L	--V---

■ Galactoside binding site

FIG. 7D